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o| |o   IntelliGenetics
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-724-107.res made by tport on Mon 4 Oct 104 14:23:17-PST.

Query sequence being compared:US-10-063-724-107 (1-2397)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

Results of the initial comparison of US-10-063-724-107 (1-2397) with:
        File : US09830328C.seq

100-
   -
 N -
 U 50-
 M -
 B -
 E -
 R -
   -
 O -
 F 10-
   -
 S -
 E 5-
 Q -
 U -
 E -
 N -* 
 C -
 E -                                                                    *
 S 0-
   ------|----|----|----|----|----|----|----|----|----|----|----|----|
SCORE 0  266  532  798 1064 1331 1597 1863 2129 2395
STDEV 0    0                   1    1

                    PARAMETERS

Similarity matrix    Unitary
Mismatch penalty     1        K-tuple            4
Gap penalty          5.00     Joining penalty    30
Gap size penalty     0.33     Window size        500
Cutoff score         1
Randomization group  0

                SEARCH STATISTICS

Scores:          Mean      Median      Standard Deviation
                 836       57          1349.85

Times:           CPU                   Total Elapsed
                 00:00:00.00           00:00:00.00

Number of residues:             6063
Number of sequences searched:   3
Number of scores above cutoff:  3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                          Init.  Opt.
Sequence Name     Description                           Length Score Score Sig. Frame
-----------------------------------------------------------------------------------------
                  **** 1 standard deviation above mean ****
1. US-09-830-328C-4 Sequence 4, Application U  2768  2395  2395  1.15   0

1. US-10-063-724-107 (1-2397)
   US-09-830-328C-4 Sequence 4, Application US/09830328C

Initial Score   = 2395   Optimized Score  = 2395   Significance   = 1.15
Residue Identity = 99%    Matches          = 2395   Mismatches     = 2
Gaps             = 0      Conservative Substitutions = 0

                         X        10        20
                  AGAGAAGAAGAGCGTCCAGCT
                  AGAGAAGAAGAGAGAAAGAAGAGCGTCCAGCT
          TTTTTTCTTTTTCCCAGAGGCGGCGGCGGCGGGGGGGGAGAGAAAGAAGAGCGTCCAGCT
          320       330       340       350    360 X    370       380

                   30        40        50        60        70        80        90
          GAAGCCAATGCAGCCCTCCGGCTCTCCGCGGAAGAGAAGTTCCTGCCCGATGAGCCCGCGTGCGTCCCCG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GAAGCCAATGCAGCCCTCCGGCTCTCCGCGGAAGAGAAGTTCCTGCCCGATGAGCCCGCGTGCGTCCCCG
          390       400       410       420       430       440       450

                   100       110       120       130       140       150       160
          ACTATCCCCAGGCGGCGGTGGGCACCGGGCCCAGGGCCGACGATCGCTGCGTTTTGCCCTTGGGAGTAGG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ACTATCCCCAGGCGGCGGTGGGCACCGGGCCCAGGGCCGACGATCGCTGCGTTTTGCCCTTGGGAGTAGG
          460       470       480       490       500       510       520

                   170       180       190       200       210       220       230
          ATGTGGTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCACATGGCAGAGAAGATTCCGTGAAGTGTCTGC
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ATGTGGTGAAAGGATGGGGCTTCTCCCTTACGGGGCTCACATGGCAGAGAAGATTCCGTGAAGTGTCTGC
          530       540       550       560       570       580       590

                   240       250       260       270       280       290       300  310
          GCTGCCTGCTCACGGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GCTGCCTGCTCACGGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGGA
          600       610       620       630       640       650       660       670

                   320       330       340       350       360       370       380
          TGAGGGACTACCTAAATAATGTTCCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TGAGGGACTACCTAAATAATGTTCCACTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTCATTTTGACTT
          680       690       700       710       720       730       740

                   390       400       410       420       430       440       450
          ACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGATGTTAGGATATT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ACTTTCCTGTGGTTCATCCGGTCATGATTGCTGTTTGCTGTTTCCTTATCATTGTGGGATGTTAGGATATT
          750       760       770       780       790       800       810

                   460       470       480       490       500       510       520
          GTGGACGGTGAAAGAAATCTGTTGCTTCTTGCTACTTGAAGTTTGCTTGTCATTTTCTGTGTAG
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          GTGGACGGTGAAAGAAATCTGTTGCTTCTTGCTACTTGAAGTTTGCTTGTCATTTTCTGTGTAG
          820       830       840       850       860       870       880

                   530       540       550       560       570       580       590
          AACTGGCTTGTGCGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          AACTGGCTTGTGCGCGTTTGGACATATGAACAGGAACTTATGGTTCCAGTACAATGGTCAGATATGGTCACTT
          890       900       910       920       930       940       950

                   600       610       620       630       640       650       660  670
          TGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGA
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          TGAAAGCCAGGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGA
          960       970       980       990       1000      1010      1020      1030
```

```
                  1540      1550      1560      1570      1580      1590      1600
        TTAGAAAATACTAATAACTTTTATTACTTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAA
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TTAGAAAATACTAATAACTTTTATTACTTACTCAGCGATCTATTCTTCTGATGCTAAATAAATTATATATCAGAAA
                  1900      1910      1920      1930      1940      1950      1960

                  1610      1620      1630      1640      1650      1660      1670
        ACTTTCAATATTGGTGACTACCTAAATGTGATTTTGCTGGTTACTAAAAATATTCTTACCACTTAAAAGAGAGC
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        ACTTTCAATATTGGTGACTACCTAAATGTGATTTTGCTGGTTACTAAAAATATTCTTACCACTTAAAAGAGAGC
                  1970      1980      1990      2000      2010      2020      2030

                  1680      1690      1700      1710      1720      1730      1740      1750
        AAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTGTATATAAGTCTGTGTTAAATCGTGTATAATCGTGTATAATTCAG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        AAGCTAACACATTGTCTTAAGCTGATCAGGGATTTTTGTATAATAAGTCATGTATAATGTCTGTGTTAAATCGTGTATAATTCAG
                  2040      2050      2060      2070      2080      2090      2100      2110
                                                                              1810      1820

                  1760      1770      1780      1790      1800      1810      1820
        TCGATTTCAGTTCTGATAATGTTAAGATAACCATTATGAAAAGGAGAAAATTGTCCTGTATAGCATCATTAT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TCGATTTCAGTTCTGATAATGTTAAGATAACCATTATGAAAAGGAGAAAATTGTCCTGTATAGCATCATTAT
                  2120      2130      2140      2150      2160      2170      2180

                  1830      1840      1850      1860      1870      1880      1890
        TTTAGCCCTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGCTTATATTACACATATAAACTGTATTTTA
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TTTAGCCCTTCCTGTTAATAAAGCTTTACTATTCTGTCCTGGCTTATATTACACATATAAACTGTATTTTA
                  2190      2200      2210      2220      2230      2240      2250

                  1900      1910      1920      1930      1940      1950      1960
        AATACTTAACCACTAATTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTC
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        AATACTTAACCACTAATTTGAAAATTACCAGTGTGATACATAGGAATCATTATTCAGAATGTAGTCTGGTC
                  2260      2270      2280      2290      2300      2310      2320

                  1970      1980      1990      2000      2010      2020      2030
        TTTAGGAGTATTAATAAGAAAATTTGCACATAACCTAGTGATTCAGAAGGACTTGTATGCTGTGTTTTCT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TTTAGGAGTATTAATAAGAAAATTTGCACATAACCTAGTGATTCAGAAGGACTTGTATGCTGTGTTTTCT
                  2330      2340      2350      2360      2370      2380      2390

                  2040      2050      2060      2070      2080      2090      2100      2110
        CCCAAATGAAGACTCTTTTGCACCTAAACACTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAGC
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        CCCAAATGAAGACTCTTTTGCACCTAAACACTTTTAAAAAGCTTATCTTTGCCTTCTCCAAACAAGAGC
                  2400      2410      2420      2430      2440      2450      2460      2470

                  2120      2130      2140      2150      2160      2170      2180
        AATAGTCTCCAAGTCAATATAAATTCTACAGAAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAAT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        AATAGTCTCCAAGTCAATATAAATTCTACAGAAAAATAGTGTTCTTTTTCTCCAGAAAAATGCTTGTGAGAAT
                  2480      2490      2500      2510      2520      2530      2540

                  2190      2200      2210      2220      2230      2240      2250
        CATTAAAACATGTGACAATTTAGAGATTCTTTGTTTATTTCACTGATTAATAATACTGTGGCAAATTACACA
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        CATTAAAACATGTGACAATTTAGAGATTCTTTGTTTATTTCACTGATTAATAATACTGTGGCAAATTACACA
                  2550      2560      2570      2580      2590      2600      2610

                  2260      2270      2280      2290      2300      2310      2320
        GATTATTAAATTTTTTACAAGAGTATAGTAGTATATTTATTTGAAAATGGGAAAAGTGCATTTTACTGTATTTTG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GATTATTAAATTTTTTACAAGAGTATAGTAGTATATTTATTTGAAAATGGGAAAAGTGCATTTTACTGTATTTTG
                  2620      2630      2640      2650      2660      2670      2680

                  2330      2340      2350      2360      2370      2380      2390
        TGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAAATTAAAATGTCTCAAGTAAATATTTTCTAGAGAGTAA  X
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  X
        TGTATTTTGTTTATTTCTCAGAATATGGAAAGAAAAATTAAAATGTCTCAAGTAAATATTTTCTAGAGAGTAA
                  2690      2700      2710      2720      2730      2740      2750

        AAAAAAAAA
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                  680       690       700       710       720       730       740
        GAGAGTTTAAGTGCTGTGGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGGATGGACTGGCCCCCAG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GAGAGTTTAAGTGCTGTGGGAGTAGTATATTTCACTGACTGGTTGGAAATGACAGAGGATGGACTGGCCCCCAG
                  1040      1050      1060      1070      1080      1090      1100

                  750       760       770       780       790       800       810
        ATTCCTGCTGTGTTAGAGAATTCCCAAACAGGGCCCACCAGGAGATCTCAGTGACCTTTATC
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        ATTCCTGCTGTGTTAGAGAATTCCCAAACAGGGCCCACCAGGAGATCTCAGTGACCTTTATC
                  1110      1120      1130      1140      1150      1160      1170

                  820       830       840       850       860       870       880
        AAGAGGGTGTGGGAGAAAATGTATTCCTTTTGAGAGGAACCAAACACTGCAGGTGCTGAGGTTTCTGG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        AAGAGGGTGTGGGAGAAAATGTATTCCTTTTGAGAGGAACCAAACACTGCAGGTGCTGAGGTTTCTGG
                  1180      1190      1200      1210      1220      1230      1240

                  890       900       910       920       930       940       950
        GAATCTCCATTGGGGTGACACAAATCCTGGCCATGAATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GAATCTCCATTGGGGTGACACAAATCCTGGCCATGAATTCTCACCATTACTCTGCTCTGGGCTCTGTATTATG
                  1250      1260      1270      1280      1290      1300      1310

                  960       970       980       990       1000      1010      1020      1030
        ATAGAAGGAGGAGCCTGGGACAGACCAAATGAGTCCTTGAAGGAATGGACAACTCTCAGCACCTGTCATGTCCCT
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        ATAGAAGGAGGGACGCCGGGACAGACCAAATGAGTCCTTGAAGGAATGGACAACTCTCAGCACCTGTCATGTCCCT
                  1320      1330      1340      1350      1360      1370      1380      1390

                  1040      1050      1060      1070      1080      1090      1100
        CAGTAGAACTGTTGAAACCAAGCCTGTCAGAGAATCTTGAACCACCATCCATGGCAAACAGCTTAATACAC
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        CAGTAGAACTGTTGAAACCAAGCCTGTCAGAGAATCTTGAACCACCATCCATGGCAAACAGCTTAATACAC
                  1400      1410      1420      1430      1440      1450      1460

                  1110      1120      1130      1140      1150      1160      1170
        ACTTTGAGATGGAGATCGGAGGAGTTATAAAAGAAATGTCACAGAAGAAACCACAAAACTTGTTTTATTGGACTTGTG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        ACTTTGAGATGGAGATCGGAGGAGTTATAAAAGAAATGTCACAGAAGAAACCACAAAACTTGTTTTATTGGACTTGTG
                  1470      1480      1490      1500      1510      1520      1530

                  1180      1190      1200      1210      1220      1230      1240
        AATTTTGAGTACATACTATGTGTTCAGAGAAATATGTAGAAATAAAAATGTGCCATAAAAATAACACCTAAG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        AATTTTGAGTACATACTATGTGTTCAGAGAAATATGTAGAAATAAAAATGTGCCATAAAAATAACACCTAAG
                  1540      1550      1560      1570      1580      1590      1600

                  1250      1260      1270      1280      1290      1300      1310
        CATATTACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTCATGTCATAAGTCACCACCTGGACAATAATT
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        CATATTACTATTCTATGCTTTAAAATGAGGATGGAAAAGTTCATGTCATAAGTCACCACCTGGACAATAATT
                  1610      1620      1630      1640      1650      1660      1670

                  1320      1330      1340      1350      1360      1370      1380      1390
        GATGCCCTTAAAATGCTGAAGACACGAGATGTCATACCCACTGTGTAGCCTGTAGCCTGTATGACTTTACTGAACACAG
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GATGCCCTTAAAATGCTGAAGACACGAGATGTCATACCCACTGTGTAGCCTGTAGCCTGTATGACTTTACTGAACACAG
                  1680      1690      1700      1710      1720      1730      1740      1750

                  1400      1410      1420      1430      1440      1450      1460
        TTATGTTTGAGGCAGCAGCATGTTGATTAGCATTCCGCATCCATGCAAACGAGTCACATATGGGGACTG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        TTATGTTTGAGGCAGCAGCATGTTGATTAGCATTCCGCATCCATGCAAACGAGTCACATATGGGGACTG
                  1760      1770      1780      1790      1800      1810      1820

                  1470      1480      1490      1500      1510      1520      1530
        GAGCCATAGTAGTAAAGGTTGATTTACTTCTCACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAG
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
        GAGCCATAGTAGTAAAGGTTGATTTACTTCTCACCAACTAGTATATAAAGTACTAATTAAATGCTAACATAGGAAG
                  1830      1840      1850      1860      1870      1880      1890
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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq1382andSeq4.res made by tport on Wed 15 Sep 104 14:43:39-PST.

Query sequence being compared:us100407391382 (1-442)
Number of sequences searched:                3
Number of scores above cutoff:               3

Results of the initial comparison of us100407391382 (1-442) with:
       File : US09830328C.seq
```

```
100-
      |
      |
   50-
N     |
U     |
M     |
B     |
E     |
R  10-|
O     |
F   5-|
S     |
C     |
O     |
R     |
E   0-|                                                    *
S     |-----------------------------------------------------------
        **
SCORE  0    46    92   138   184   231   277   323   369   415
STDEV       0                            1
```

```
                PARAMETERS

Similarity matrix    Unitary
Mismatch penalty       1        K-tuple              4
Gap penalty          5.00       Joining penalty     30
Gap size penalty     0.33       Window size        442
Cutoff score           1
Randomization group    0

                SEARCH STATISTICS

              Mean     Median    Standard Deviation
Scores:       159       29          221.72

                CPU                 Total Elapsed
Times:    00:00:00.00               00:00:00.00

Number of residues:             6063
Number of sequences searched:      3
Number of scores above cutoff:     3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                                  Init.  Opt.
Sequence Name   Description                              Length  Score  Score  Sig.  Frame
--------------  --------------------                     ------  -----  -----  ----  -----
                **** 1 standard deviation above mean ****
  1. US-09-830-328C-4 Sequence 4, Application U          2768    415    419    1.15    0


1. us100407391382 (1-442)
   US-09-830-328C-4 Sequence 4, Application US/09830328C

Initial Score     =  415      Optimized Score      =  419      Significance =  1.15
Residue Identity  =  96%      Matches              =  425      Mismatches   =  13
Gaps              =   3       Conservative Substitutions =  4                 0

            X        10        20
       GAATTCGGCCAAAGAGAGGCCTAG
          ||| |||||||||||||||||||
GGATGACAAATTATGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAATTTTTTTCAGAGAG----AG
970       980       990       1000      1010      1020      1030

            30        40        50        60        70        80        90
       TTTAAGTGCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TTTAAGTGCTGTGGAGTAGTATATTCACTGACTGGTTGGAAATGACAGAGATGGACTGGCCCCCAGATTCC
1040      1050      1060      1070      1080      1090      1100

            100       110       120       130       140       150       160
       TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TGCTGTGTTAGAGAATTCCCAGGATGTTCCAAACAGGCCCACCAGGAAGATCTCAGTGACCTTTATCAAGAG
1110      1120      1130      1140      1150      1160      1170      1180

            170       180       190       200       210       220       230
       GGTTGTGGGAAGAAAAATGTATTCCTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATC
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       GGTTGTGGGAAGAAAAATGTATTCCTTTTGAGAGGAACCAAACAACTGCAGGTGCTGAGGTTTCTGGGAATC
1190      1200      1210      1220      1230      1240      1250

           -240       250       260       270       280       290       300       310
       TCCATTGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTCGGGCTCTGTATTATGATAGA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TCCATTGGGTGACACAAATCCTGGCCATGATTCTCACCATTACTCTGCTCTCGGGCTCTGTATTATGATAGA
1260      1270      1280      1290      1300      1310      1320

            320       330       340       350       360       370       380
       AGGGAGCCTGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCTCAGTA
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       AGGGAGCCGCGGGACAGACCAAATGATGTCCTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCTCAGTA
1330      1340      1350      1360      1370      1380      1390

            390       400       410       420       430       440  X
       GAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACCTGAG
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
       GAACTGTTGAAACCAAGCCTGTCAAGAATCTTTGAACACACATCCATGGCAAACCTTTAATACACACTTT
1400      1410      1420      1430      1440      1450      1460

       GAGATGGAGGAGTTATAAAAAGAAATGTCACAGAAGAA
1470      1480      1490      1500
```

us-10-063-724-107.res

Mon Oct 4 14:28:27 2004
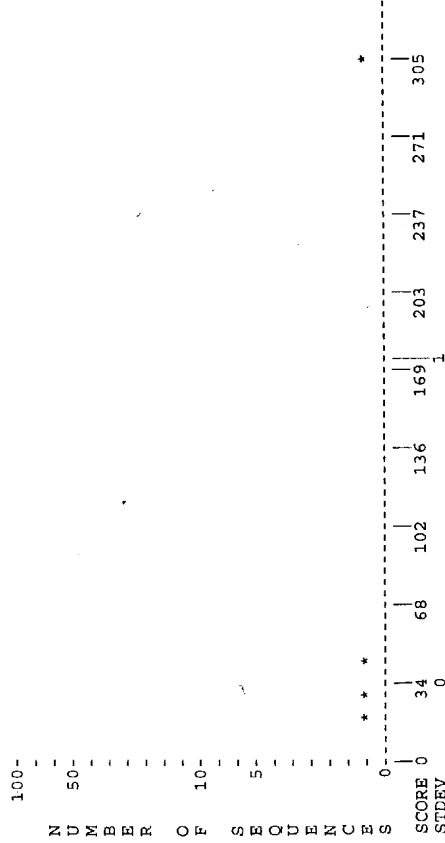
2760

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 O||O   IntelliGenetics
 > O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-724-108.res made by tport on Mon 4 Oct 104 14:27:06-PST.

Query sequence being compared:US-10-063-724-108 (1-305)
Number of sequences searched:           4
Number of scores above cutoff:          4

        Results of the initial comparison of US-10-063-724-108 (1-305) with:
        File : US09830328C.pep

     100-
        -
   N    -
   U 50-
   M    -
   B    -
   E    -
   R    -
        -
   O    -
   F 10-
        -
   S    -
   E  5-
   Q    -
   U    -
   E    -
   N    -                                                                *
   C    -
   E    *    *
   S  0-----*-----------------------------------------------------------|----
 SCORE 0   34   68   102   136   169   203   237   271   305
 STDEV 0    0                     1
```

                        PARAMETERS

Similarity matrix   PAM-150   K-tuple   1
Threshold level of sim. 16%   Joining penalty   20
Mismatch penalty   1   Window size   305
Gap penalty   5.00
Gap size penalty   0.05
Cutoff score   1
Randomization group   0

                   SEARCH STATISTICS

Scores: Mean   Median   Standard Deviation
               101   33   136.13

Times: CPU   Total Elapsed
               00:00:00.00   00:00:00.00

Number of residues: 1078
Number of sequences searched: 4
Number of scores above cutoff: 4

1. US-10-063-724-108 (1-305)
   US-09-830-328C-2 Sequence 2, Application US/09830328C

Initial Score   = 305   Optimized Score = 305   Significance = 1.50
Residue Identity = 100%   Matches   = 305   Mismatches   = 0
Gaps   = 0   Conservative Substitutions = 0

```
        X        10        20        30        40        50        60        70
        |    O  < |         |         |         |         |         |         |
 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMIAVCC
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTLTAETRVEEAVILTYFPVVHPVMIAVCC
        X        10        20        30        40        50        60        70

                 80        90       100       110       120       130       140
                  |         |         |         |         |         |         |
 FLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVTLKARMTNYGLPRYR
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 FLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQWSDMVTLKARMTNYGLPRYR
                 80        90       100       110       120       130       140

                150       160       170       180       190       200       210
                  |         |         |         |         |         |         |
 WLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 WLTHAWNFFQREFKCCGVVYFTDWLEMTEMDWPPDSCCVREFPGCSKQAHQEDLSDLYQEGCGKKMYSFLRG
                150       160       170       180       190       200       210

                220       230       240       250       260       270       280
                  |         |         |         |         |         |         |
 TKQLQVLRFLGISIGVTQILAMLTITLLWALYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFE
 |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 TKQLQVLRFLGISIGVTQILAMLTITLLWALYDRREPGTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFE
                220       230       240       250       260       270       280

                290       300        X
                  |         |
 HTSMANSFNTHFEMEEL
 |||||||||||||||||
 HTSMANSFNTHFEMEEL
                290       300        X
```